IN THE SPECIFICATION

Please amend the specification of the application as follows:

On page 57, please amend paragraph [0133] as follows:

[0133] As understood by one of ordinary skill in the art, the sequence of a cloned cDNA insert obtained, may be compared against public databases such as Genbank to discern any identity or homology to known sequences. Programs, such BLAST, for performing such a search are available on the National Center for Biotechnology Information's web page ~~located at~~ http://www.ncbi.nlm.nih.gov. The results from Genbank search may reveal the potential function of a polypeptide or RNA molecule encoded by the cDNA. In addition to searching gene sequence database, the use of commercially available analysis software is well known in the art. For example, software packages such as the Wisconsin Package™ (Genetic Computer Group, Madison, Wisconsin) include programs such as FRAMES and CodonPreference that help to identify protein coding sequences in a query nucleotide sequence. FRAMES displays open reading frames for the six DNA translation frames, allowing one to quickly assess the presence or absence of stretches of open-reading frames that are likely to be protein encoding regions. CodonPreference is a more sophisticated program that identifies and displays possible protein coding regions based on similarity of the codon usage in the sequence to a codon frequency table (Gribskov et al., 1984).

On page 66, please amend paragraph [0155] as follows:

[0155] To confirm the fluctuation in lea transcript levels by Northern analysis. RNA was extracted from zygotic embryos at different stages of development. A pine

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'dehydrin' cDNA from the North Carolina State University cDNA collection ~~(http://www.cbc.med.umn.edu/ResearchProjects/Pine/DOE.pine/index.html)~~ was used as probe for some experiments. Dehydrins are a class of lea protein, originally identified as water deficit inducible proteins. Since the expression of this class of protein is well characterized, in contrast to our lea genes, the dehydrin expression profile could act as a reference point. After probing with dehydrin, blots were stripped and probed with a 26S rDNA probe from Arabidopsis to check the loading of the original gel. The normalized expression pattern of dehydrin in the zygotic embryogenesis is illustrated in the top panel of Figure 4. The expression of the dehydrin gene was induced at stage 5 and reached a peak at stage 6. It declined at stage 7 - 8, just prior to the onset of the desiccation. Then the mRNAs level remained low from stage 9.1 through 9.5. The dehydrin mRNA levels rose again late in development, from stage 9.6 on, apparently dropping in very late development. A similar pattern of expression was observed in a parallel experiment when our lea-like clone, LPZ-216, was used as a probe.

On page 77, please amend paragraph [0178] as follows:

[0178] For the following example analysis RNA was isolated from embryos at different stages in development, early stage somatic embryos and late-stage somatic embryos. The cDNA probes used in this example are not contained in the SEQ ID NOS: 1-327, but rather, are generic, publicly available pine sequences obtained from the Pine Gene Discovery project ~~located at (http://www.cbc.med.umn.edu/ResearchProjects/Pine/DOE.pine/index.html)~~.

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These clones are homologs to the well-studied *Arabidopsis* genes that have been shown to have significant influence on embryo development in this plant. The pine clone names (first column) and corresponding references for the *Arabidopsis* homologs are shown in Table 4. The three clones listed, *Lec*, *Lie*, and *Pkl*, are for representative purposes within this example and it will be clear to one skilled in the art that any of the SEQ ID NOS: 1-327 could be substituted for those here as all will help identify conditions for improved performance in culture.

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